



#4

# SEQUENCE LISTING

<110> Boetsch, Paul W.  
Avery, Angela M.  
Kaur, Balveen

<120> Broad Specificity DNA Damage Endonuclease

<130> 25-98A

<140> US/09/724,296

<141> 2000-11-28

<150> US/09/327,984

<151> 1999-06-08

<150> US/60/088,521

<151> 1998-06-08

<150> US/60/134,752

<151> 1999-05-18

<160> 71

<170> PatentIn Ver. 2.0

<210> 1

<211> 2492

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Coding  
sequence for fusion protein of GST signal peptide  
and the UVDE protein of Schizosaccharomyces pombe

<400> 1

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tattgatggt gatgttaaat taacacagtc tatggccatc atacgttata tagctgacaa 240
gcacaacatg ttggttgggt gtccaaaaga gcgtgcagag atttcaatgc ttgaaggagc 300
ggttttggat attagatacg gtgtttcgag aattgcatat agtaaagact ttgaaactct 360
caaagttgat tttcttagca agctacctga aatgctgaaa atgttcgaag atcgtttatg 420
tcataaaaca tatttaaatt ttgacctgt aaccatcct gacttcattg tgtatgacgc 480
tcttgatgtt gttttataca tggacccaat gtgcctggat gcgttcccaa aattagtttg 540
ttttaaaaaa cgtattgaag ctatcccaca aattgataag tacttgaaat ccagcaagta 600
tatagcatgg cctttgcagg gctggcaagc caggtttggt ggtggcgacc atcctccaaa 660
atcgatcat ctggttccgc gtggatccat gcttaggcta ttgaaacgaa atattcaaat 720
ctctaaacgc attgttttca ccatattaaa acaaaaggca tttaaaggta atcatccttg 780
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gggaattaca cagaagcaac attactcaga atcggtgat ccaacggcga tttctgggat 2220
gaaacgacgt gctcactctg atagggtgtt tgactttcca ccgtgtgatc ctacaatgga 2280
tctaataata gaagctaagg aaaaggaaca ggctgtatgt gaattgtgta gacgttatga 2340
gttacaaaat ccaccatgtc ctcttgaaat tatggggcct gaatacgatc aaactcgaga 2400
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<210> 2

<211> 828

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion protein  
of GST leader peptide and Schizosaccharomyces  
pombe UVDE

<400> 2

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Met Thr Lys Leu Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val
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Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu
      20             25             30

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His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe
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Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp
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Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys  
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His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met  
85 90 95

Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala  
100 105 110

Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu  
115 120 125

Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr  
130 135 140

Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala  
145 150 155 160

Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro  
165 170 175

Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp  
180 185 190

Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp  
195 200 205

Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp His Leu  
210 215 220

Val Pro Arg Gly Ser Met Leu Arg Leu Leu Lys Arg Asn Ile Gln Ile  
225 230 235 240

Ser Lys Arg Ile Val Phe Thr Ile Leu Lys Gln Lys Ala Phe Lys Gly  
245 250 255

Asn His Pro Cys Val Pro Ser Val Cys Thr Ile Thr Tyr Ser Arg Phe  
260 265 270

His Cys Leu Pro Asp Thr Leu Lys Ser Leu Leu Pro Met Ser Ser Lys  
275 280 285

Thr Thr Leu Ser Met Leu Pro Gln Val Asn Ile Gly Ala Asn Ser Phe  
290 295 300

Ser Ala Glu Thr Pro Val Asp Leu Lys Lys Glu Asn Glu Thr Glu Leu  
305 310 315 320

Ala Asn Ile Ser Gly Pro His Lys Lys Ser Thr Ser Thr Ser Thr Arg  
325 330 335

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Lys Arg Ala Arg Ser Ser Lys Lys Lys Ala Thr Asp Ser Val Ser Asp  
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 Lys Ile Asp Glu Ser Val Ala Ser Tyr Asp Ser Ser Thr His Leu Arg  
 355 360 365  
 Arg Ser Ser Arg Ser Lys Lys Pro Val Asn Tyr Asn Ser Ser Ser Glu  
 370 375 380  
 Ser Glu Ser Glu Glu Gln Ile Ser Lys Ala Thr Lys Lys Val Lys Gln  
 385 390 395 400  
 Lys Glu Glu Glu Glu Tyr Val Glu Glu Val Asp Glu Lys Ser Leu Lys  
 405 410 415  
 Asn Glu Ser Ser Ser Asp Glu Phe Glu Pro Val Val Pro Glu Gln Leu  
 420 425 430  
 Glu Thr Pro Ile Ser Lys Arg Arg Arg Ser Arg Ser Ser Ala Lys Asn  
 435 440 445  
 Leu Glu Lys Glu Ser Thr Met Asn Leu Asp Asp His Ala Pro Arg Glu  
 450 455 460  
 Met Phe Asp Cys Leu Asp Lys Pro Ile Pro Trp Arg Gly Arg Leu Gly  
 465 470 475 480  
 Tyr Ala Cys Leu Asn Thr Ile Leu Arg Ser Met Lys Glu Arg Val Phe  
 485 490 495  
 Cys Ser Arg Thr Cys Arg Ile Thr Thr Ile Gln Arg Asp Gly Leu Glu  
 500 505 510  
 Ser Val Lys Gln Leu Gly Thr Gln Asn Val Leu Asp Leu Ile Lys Leu  
 515 520 525  
 Val Glu Trp Asn His Asn Phe Gly Ile His Phe Met Arg Val Ser Ser  
 530 535 540  
 Asp Leu Phe Pro Phe Ala Ser His Ala Lys Tyr Gly Tyr Thr Leu Glu  
 545 550 555 560  
 Phe Ala Gln Ser His Leu Glu Glu Val Gly Lys Leu Ala Asn Lys Tyr  
 565 570 575  
 Asn His Arg Leu Thr Met His Pro Gly Gln Tyr Thr Gln Ile Ala Ser  
 580 585 590  
 Pro Arg Glu Val Val Val Asp Ser Ala Ile Arg Asp Leu Ala Tyr His  
 595 600 605

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Asp Glu Ile Leu Ser Arg Met Lys Leu Asn Glu Gln Leu Asn Lys Asp  
610 615 620

Ala Val Leu Ile Ile His Leu Gly Gly Thr Phe Glu Gly Lys Lys Glu  
625 630 635 640

Thr Leu Asp Arg Phe Arg Lys Asn Tyr Gln Arg Leu Ser Asp Ser Val  
645 650 655

Lys Ala Arg Leu Val Leu Glu Asn Asp Asp Val Ser Trp Ser Val Gln  
660 665 670

Asp Leu Leu Pro Leu Cys Gln Glu Leu Asn Ile Pro Leu Val Leu Asp  
675 680 685

Trp His His His Asn Ile Val Pro Gly Thr Leu Arg Glu Gly Ser Leu  
690 695 700

Asp Leu Met Pro Leu Ile Pro Thr Ile Arg Glu Thr Trp Thr Arg Lys  
705 710 715 720

Gly Ile Thr Gln Lys Gln His Tyr Ser Glu Ser Ala Asp Pro Thr Ala  
725 730 735

Ile Ser Gly Met Lys Arg Arg Ala His Ser Asp Arg Val Phe Asp Phe  
740 745 750

Pro Pro Cys Asp Pro Thr Met Asp Leu Met Ile Glu Ala Lys Glu Lys  
755 760 765

Glu Gln Ala Val Phe Glu Leu Cys Arg Arg Tyr Glu Leu Gln Asn Pro  
770 775 780

Pro Cys Pro Leu Glu Ile Met Gly Pro Glu Tyr Asp Gln Thr Arg Asp  
785 790 795 800

Gly Tyr Tyr Pro Pro Gly Ala Glu Lys Arg Leu Thr Ala Arg Lys Arg  
805 810 815

Arg Ser Arg Lys Glu Glu Val Glu Glu Asp Glu Lys  
820 825

<210> 3  
<211> 1161  
<212> DNA  
<213> Schizosaccharomyces pombe

<220>  
<221> misc\_feature  
<222> (1)..(1161)

<223> DNA sequence encoding UVDE protein, truncated at amino acid residue 228.

<400> 3

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ggtacgcaaa atgttttaga tttaatcaaa ttggttgagt ggaatcacia ctttggcatt 240
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<210> 4

<211> 371

<212> PRT

<213> Schizosaccharomyces pombe

<220>

<221> VARIANT

<222> (1)..(371)

<223> Truncated version of the UVDE protein.

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```

```

Pro Trp Arg Gly Arg Leu Gly Tyr Ala Cys Leu Asn Thr Ile Leu Arg
          20              25              30

```

```

Ser Met Lys Glu Arg Val Phe Cys Ser Arg Thr Cys Arg Ile Thr Thr
          35              40              45

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Ile Gln Arg Asp Gly Leu Glu Ser Val Lys Gln Leu Gly Thr Gln Asn
          50              55              60

```

```

Val Leu Asp Leu Ile Lys Leu Val Glu Trp Asn His Asn Phe Gly Ile
          65              70              75              80

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His Phe Met Arg Val Ser Ser Asp Leu Phe Pro Phe Ala Ser His Ala  
85 90 95

Lys Tyr Gly Tyr Thr Leu Glu Phe Ala Gln Ser His Leu Glu Glu Val  
100 105 110

Gly Lys Leu Ala Asn Lys Tyr Asn His Arg Leu Thr Met His Pro Gly  
115 120 125

Gln Tyr Thr Gln Ile Ala Ser Pro Arg Glu Val Val Val Asp Ser Ala  
130 135 140

Ile Arg Asp Leu Ala Tyr His Asp Glu Ile Leu Ser Arg Met Lys Leu  
145 150 155 160

Asn Glu Gln Leu Asn Lys Asp Ala Val Leu Ile Ile His Leu Gly Gly  
165 170 175

Thr Phe Glu Gly Lys Lys Glu Thr Leu Asp Arg Phe Arg Lys Asn Tyr  
180 185 190

Gln Arg Leu Ser Asp Ser Val Lys Ala Arg Leu Val Leu Glu Asn Asp  
195 200 205

Asp Val Ser Trp Ser Val Gln Asp Leu Leu Pro Leu Cys Gln Glu Leu  
210 215 220

Asn Ile Pro Leu Val Leu Asp Trp His His His Asn Ile Val Pro Gly  
225 230 235 240

Thr Leu Arg Glu Gly Ser Leu Asp Leu Met Pro Leu Ile Pro Thr Ile  
245 250 255

Arg Glu Thr Trp Thr Arg Lys Gly Ile Thr Gln Lys Gln His Tyr Ser  
260 265 270

Glu Ser Ala Asp Pro Thr Ala Ile Ser Gly Met Lys Arg Arg Ala His  
275 280 285

Ser Asp Arg Val Phe Asp Phe Pro Pro Cys Asp Pro Thr Met Asp Leu  
290 295 300

Met Ile Glu Ala Lys Glu Lys Glu Gln Ala Val Phe Glu Leu Cys Arg  
305 310 315 320

Arg Tyr Glu Leu Gln Asn Pro Pro Cys Pro Leu Glu Ile Met Gly Pro  
325 330 335

Glu Tyr Asp Gln Thr Arg Asp Gly Tyr Tyr Pro Pro Gly Ala Glu Lys  
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052701 052701 052701

Arg Leu Thr Ala Arg Lys Arg Arg Ser Arg Lys Glu Glu Val Glu Glu  
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Asp Glu Lys  
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<210> 5  
<211> 1811  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Nucleotide  
sequence encoding fusion protein of GST signal  
peptide and the truncated version of S. pombe UVDE  
protein.

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caaagttgat tttcttagca agctacctga aatgctgaaa atgttcgaag atcgtttatg 420  
tcataaaaaca tatttaaata ttgacctagt aaccatcct gacttcatgt tgtatgacgc 480  
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<210> 6  
 <211> 600  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion protein  
 comprising the GST signal peptide and the  
 truncated UVDE protein of *S. pombe*.

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 Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu  
                           20                          25                          30  
 His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe  
                           35                          40                          45  
 Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp  
           50                          55                          60  
 Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys  
           65                          70                          75                          80  
 His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met  
                           85                          90                          95  
 Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala  
                           100                          105                          110  
 Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu  
           115                          120                          125  
 Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr  
           130                          135                          140  
 Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala  
           145                          150                          155                          160  
 Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro  
                           165                          170                          175  
 Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp  
           180                          185                          190  
 Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp  
           195                          200                          205

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Gln	Ala	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	His	Leu	210	215	220	
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Leu	Asp	Lys	Pro	Ile	Pro	Trp	Arg	Gly	Arg	Leu	Gly	Tyr	Ala	Cys	Leu	245	250	255	
Asn	Thr	Ile	Leu	Arg	Ser	Met	Lys	Glu	Arg	Val	Phe	Cys	Ser	Arg	Thr	260	265	270	
Cys	Arg	Ile	Thr	Thr	Ile	Gln	Arg	Asp	Gly	Leu	Glu	Ser	Val	Lys	Gln	275	280	285	
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His	Asn	Phe	Gly	Ile	His	Phe	Met	Arg	Val	Ser	Ser	Asp	Leu	Phe	Pro	305	310	315	320
Phe	Ala	Ser	His	Ala	Lys	Tyr	Gly	Tyr	Thr	Leu	Glu	Phe	Ala	Gln	Ser	325	330	335	
His	Leu	Glu	Glu	Val	Gly	Lys	Leu	Ala	Asn	Lys	Tyr	Asn	His	Arg	Leu	340	345	350	
Thr	Met	His	Pro	Gly	Gln	Tyr	Thr	Gln	Ile	Ala	Ser	Pro	Arg	Glu	Val	355	360	365	
Val	Val	Asp	Ser	Ala	Ile	Arg	Asp	Leu	Ala	Tyr	His	Asp	Glu	Ile	Leu	370	375	380	
Ser	Arg	Met	Lys	Leu	Asn	Glu	Gln	Leu	Asn	Lys	Asp	Ala	Val	Leu	Ile	385	390	395	400
Ile	His	Leu	Gly	Gly	Thr	Phe	Glu	Gly	Lys	Lys	Glu	Thr	Leu	Asp	Arg	405	410	415	
Phe	Arg	Lys	Asn	Tyr	Gln	Arg	Leu	Ser	Asp	Ser	Val	Lys	Ala	Arg	Leu	420	425	430	
Val	Leu	Glu	Asn	Asp	Asp	Val	Ser	Trp	Ser	Val	Gln	Asp	Leu	Leu	Pro	435	440	445	
Leu	Cys	Gln	Glu	Leu	Asn	Ile	Pro	Leu	Val	Leu	Asp	Trp	His	His	His	450	455	460	
Asn	Ile	Val	Pro	Gly	Thr	Leu	Arg	Glu	Gly	Ser	Leu	Asp	Leu	Met	Pro	465	470	475	480

Leu Ile Pro Thr Ile Arg Glu Thr Trp Thr Arg Lys Gly Ile Thr Gln  
485 490 495

Lys Gln His Tyr Ser Glu Ser Ala Asp Pro Thr Ala Ile Ser Gly Met  
500 505 510

Lys Arg Arg Ala His Ser Asp Arg Val Phe Asp Phe Pro Pro Cys Asp  
515 520 525

Pro Thr Met Asp Leu Met Ile Glu Ala Lys Glu Lys Glu Gln Ala Val  
530 535 540

Phe Glu Leu Cys Arg Arg Tyr Glu Leu Gln Asn Pro Pro Cys Pro Leu  
545 550 555 560

Glu Ile Met Gly Pro Glu Tyr Asp Gln Thr Arg Asp Gly Tyr Tyr Pro  
565 570 575

Pro Gly Ala Glu Lys Arg Leu Thr Ala Arg Lys Arg Arg Ser Arg Lys  
580 585 590

Glu Glu Val Glu Glu Asp Glu Lys  
595 600

<210> 7

<211> 688

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleotide  
sequence encoding GST signal peptide.

<400> 7

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tgataaatgg cgaaacaaaa agtttgaatt gggtttggag tttcccaatc ttccttatta 180
tattgatggg gatgttaaag taacacagtc tatggccatc atacgttata tagctgacaa 240
gcacaacatg ttggttgggt gtccaaaaga gcgtgcagag atttcaatgc ttgaaggagc 300
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caaagttgat tttcttagca agctacctga aatgctgaaa atgttcgaag atcgtttatg 420
tcataaaaaca tatttaaagt ttgaccatgt aaccatcct gacttcatgt tgtatgacgc 480
tcttgatggt gttttataca tggacccaat gtgcctggat gcgttcccaa aattagtttg 540
ttttaaaaaa cgtattgaag ctatcccaca aattgataag tacttgaaat ccagcaagta 600
tatagcatgg cctttgcagg gctggcaagc cacgtttggg ggtggcgacc atcctccaaa 660
atcgatcat ctggttccgc gtggatcc 688
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<210> 8

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid  
sequence of GST signal peptide

<400> 8

Met Thr Lys Leu Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val  
1 5 10 15

Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu  
20 25 30

His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe  
35 40 45

Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp  
50 55 60

Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys  
65 70 75 80

His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met  
85 90 95

Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala  
100 105 110

Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu  
115 120 125

Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr  
130 135 140

Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala  
145 150 155 160

Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro  
165 170 175

Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp  
180 185 190

Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp  
195 200 205

Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp His Leu  
210 215 220

Val Pro Arg Gly Ser  
225

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<210> 9  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 9  
tgaggatcca atcgttttca ttttttaatg cttagg 36

<210> 10  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 10  
ggccatgggtt atttttcac ctc 23

<210> 11  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 11  
aatgggatcc gatgatcatg ctccacga 28

<210> 12  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 12  
gggatccta tttttcatcc tcttctac 28

<210> 13  
<211> 30

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Double  
stranded oligonucleotide containing cis-syn  
cyclobutane pyrimidine dimer.

<220>  
<221> misc\_feature  
<222> (15)..(16)  
<223> At positions 15- 16, the T-T is in the form of  
cis-syn cyclobutane pyrimidine dimer.

<400> 13  
catgcctgca cgaattaagc aattcgtaat 30

<210> 14  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Undamaged  
double stranded oligonucleotide.

<400> 14  
catgcctgca cgaattaagc aattcgtaat 30

<210> 15  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Double  
stranded oligonucleotide containing cis-syn  
cyclobutane dimer at positions 21-22.

<400> 15  
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcataagct 49

<210> 16  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Double  
stranded oligonucleotide containing cis-syn  
cyclobutane pyrimidine dimer at positions 21-22.

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<400> 16  
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 17  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Double  
stranded oligonucleotide containing trans- syn 11  
cyclobutane pyrimidine dimer at positions 21-22.

<400> 17  
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 18  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Double  
stranded oligonucleotide containing a 6-4 photo  
product at position 21-22.

<400> 18  
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 19  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Double  
stranded oligonucleotide containing a Dewar  
isomer.

<400> 19  
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 20  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Double  
stranded oligonucleotide containing cisplatin DNA  
diadduct at position 16-17.

<400> 20  
tccctccttc cttccggccc tccttccct tc

32

<210> 21  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Double  
stranded oligonucleotide wherein n is uracil at  
position 21.

<220>  
<221> misc\_feature  
<222> (21)  
<223> The n at position 21 is uracil.

<400> 21  
cttgactgg atgtcggcac nagcggatac aggagca

37

<210> 22  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Double  
stranded oligonucleotide wherein n is  
dihydrouracil at position 21.

<220>  
<221> misc\_feature  
<222> (21)  
<223> At position 21, n is dihydrouracil.

<400> 22  
cttgactgg atgtcggcac nagcggatac aggagca

37

<210> 23  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Double  
stranded oligonucleotide wherein n at position 21  
represents an abasic site.

<220>  
<221> misc\_feature



<222> (21)  
 <223> At position 21, n is an abasic site.

<400> 23  
 cttggactgg atgtcggcac naggcgatac aggagca

37

<210> 24  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Double  
 stranded oligonucleotide wherein n at position 13  
 is an inosine.

<220>  
 <221> misc\_feature  
 <222> (13)  
 <223> At position 13, n is inosine.

<400> 24  
 tgcaggctcga ctnaggagga tccccgggta c

31

<210> 25  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Double  
 stranded oligonucleotide wherein n at position 13  
 is xanthine.

<220>  
 <221> misc\_feature  
 <222> (13)  
 <223> N at position 13 is xanthine.

<400> 25  
 tgcaggctcga ctnaggagga tccccgggta c

31

<210> 26  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Double  
 stranded oligonucleotide wherein n at position 21  
 is 8-oxoguanine.

<220>  
 <221> misc\_feature  
 <222> (21)  
 <223> N at position 21 is 8-oxoguanine.

<400> 26  
 cttggactgg atgtcggcac naggcgatac aggagca

37

<210> 27  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Double stranded oligonucleotide representing all 16 possible base pair mismatches at position 18 in individual preparations.

<220>  
 <221> misc\_feature  
 <222> (18)  
 <223> N at position 18 represents all 16 possible base pair mismatches.

<400> 27  
 gtacccgggg atcctccnag tcgacctgca

30

<210> 28  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Double stranded oligonucleotide containing a CA mismatched base pair at position 21.

<220>  
 <221> misc\_feature  
 <222> (21)  
 <223> N at position 21 represents C of C/A mismatched base pair.

<400> 28  
 cgtagcatg cctgcacgaa ntaagcaatt cgtaatgcat t

41

<210> 29  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence: Double stranded oligonucleotide wherein there is a C/A mismatched base pair at position 36.

<220>

<221> misc\_feature

<222> (36)

<223> N at position 36 represents a C/A mismatched base pair.

<400> 29

cgttacaagt ccgtcacgaa ttaagcaatt cgtaangcat t

41

<210> 30

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Double stranded oligonucleotide wherein n at position 31 represents a C/A mismatched base pair.

<220>

<221> misc\_feature

<222> (31)

<223> The n at position 31 represents C of C/A mismatched base pair.

<400> 30

cgttacaagt ccgtcacgaa ttaagcaatt ngtaacgcat t

41

<210> 31

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Double stranded oligonucleotide wherein n at position 26 is a C/A mismatched base pair.

<220>

<221> misc\_feature

<222> (26)

<223> N at position 26 represents a C/A mismatched base pair.

<400> 31

cgttacaagt ccgtcacgaa ttaagnaatt cgtaacgcat t

41

<210> 32  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Double stranded oligonucleotide wherein n at position 21 is a C/A mismatched base pair.

<220>

<221> misc\_feature

<222> (21)

<223> The n at position 21 represents a C/A mismatched base pair.

<400> 32

cgttacaagt ccgtcacgac ntaagcaatt cgtaacgcat t

41

<210> 33

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Double stranded oligonucleotide wherein n at position 15 represents a C/A mismatched base pair.

<220>

<221> misc\_feature

<222> (15)

<223> The n at position 15 represents a C/A mismatched base pair.

<400> 33

cgttacaagt ccgtnacgaa ttaagcaatt cgtaacgcat t

41

<210> 34

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Double stranded oligonucleotide wherein n at position 10 is a C/A mismatched base pair.

<220>

<221> misc\_feature

<222> (10)

<223> The n at position 10 represents a C/A mismatched base pair.

<400> 34  
cggtacaagn ccgtcacgaa ttaagcaatt cgtaacgcat t

41

<210> 35  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Double stranded oligonucleotide wherein n at position 5 is a C/A mismatched base pair.

<220>  
<221> misc\_feature  
<222> (5)  
<223> The n at position 5 represents a C/A mismatched base pair.

<400> 35  
cgttncaggt ccgtcacgaa ttaagcaatt cgtaacgcat t

41

<210> 36  
<211> 656  
<212> PRT  
<213> Neurospora crassa

<400> 36  
Met Pro Ser Arg Lys Ser Lys Ala Ala Ala Leu Asp Thr Pro Gln Ser  
1 5 10 15  
Glu Ser Ser Thr Phe Ser Ser Thr Leu Asp Ser Ser Ala Pro Ser Pro  
20 25 30  
Ala Arg Asn Leu Arg Arg Ser Gly Arg Asn Ile Leu Gln Pro Ser Ser  
35 40 45  
Glu Lys Asp Arg Asp His Glu Lys Arg Ser Gly Glu Glu Leu Ala Gly  
50 55 60  
Arg Met Met Gly Lys Asp Ala Asn Gly His Cys Leu Arg Glu Gly Lys  
65 70 75 80  
Glu Gln Glu Glu Gly Val Lys Met Ala Ile Glu Gly Leu Ala Arg Met  
85 90 95  
Glu Arg Arg Leu Gln Arg Ala Thr Lys Arg Gln Lys Lys Gln Leu Glu  
100 105 110

Glu Asp Gly Ile Pro Val Pro Ser Val Val Ser Arg Phe Pro Thr Ala  
 115 120 125  
 Pro Tyr His His Lys Ser Thr Asn Ala Glu Glu Arg Glu Ala Lys Glu  
 130 135 140  
 Pro Val Leu Lys Thr His Ser Lys Asp Val Glu Arg Glu Ala Glu Ile  
 145 150 155 160  
 Gly Val Asp Asp Val Val Lys Met Glu Pro Ala Ala Thr Asn Ile Ile  
 165 170 175  
 Glu Pro Glu Asp Ala Gln Asp Ala Ala Glu Arg Gly Ala Ala Arg Pro  
 180 185 190  
 Pro Ala Val Asn Ser Ser Tyr Leu Pro Leu Pro Trp Lys Gly Arg Leu  
 195 200 205  
 Gly Tyr Ala Cys Leu Asn Thr Tyr Leu Arg Asn Ala Lys Pro Pro Ile  
 210 215 220  
 Phe Ser Ser Arg Thr Cys Arg Met Ala Ser Ile Val Asp His Arg His  
 225 230 235 240  
 Pro Leu Gln Phe Glu Asp Glu Pro Glu His His Leu Lys Asn Lys Pro  
 245 250 255  
 Asp Lys Ser Lys Glu Pro Gln Asp Glu Leu Gly His Lys Phe Val Gln  
 260 265 270  
 Glu Leu Gly Leu Ala Asn Ala Arg Asp Ile Val Lys Met Leu Cys Trp  
 275 280 285  
 Asn Glu Lys Tyr Gly Ile Arg Phe Leu Arg Leu Ser Ser Glu Met Phe  
 290 295 300  
 Pro Phe Ala Ser His Pro Val His Gly Tyr Lys Leu Ala Pro Phe Ala  
 305 310 315 320  
 Ser Glu Val Leu Ala Glu Ala Gly Arg Val Ala Ala Glu Leu Gly His  
 325 330 335  
 Arg Leu Thr Thr His Pro Gly Gln Phe Thr Gln Leu Gly Ser Pro Arg  
 340 345 350  
 Lys Glu Val Val Glu Ser Ala Ile Arg Asp Leu Glu Tyr His Asp Glu  
 355 360 365  
 Leu Leu Ser Leu Leu Lys Leu Pro Glu Gln Gln Asn Arg Asp Ala Val  
 370 375 380

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Met	Ile	Ile	His	Met	Gly	Gly	Gln	Phe	Gly	Asp	Lys	Ala	Ala	Thr	Leu	385	390	395	400
Glu	Arg	Phe	Lys	Arg	Asn	Tyr	Ala	Arg	Leu	Ser	Gln	Ser	Cys	Lys	Asn	405	410	415	
Arg	Leu	Val	Leu	Glu	Asn	Asp	Asp	Val	Gly	Trp	Thr	Val	His	Asp	Leu	420	425	430	
Leu	Pro	Val	Cys	Glu	Glu	Leu	Asn	Ile	Pro	Met	Val	Leu	Asp	Tyr	His	435	440	445	
His	His	Asn	Ile	Cys	Phe	Asp	Pro	Ala	His	Leu	Arg	Glu	Gly	Thr	Leu	450	455	460	
Asp	Ile	Ser	Asp	Pro	Lys	Leu	Gln	Glu	Arg	Ile	Ala	Asn	Thr	Trp	Lys	465	470	475	480
Arg	Lys	Gly	Ile	Lys	Gln	Lys	Met	His	Tyr	Ser	Glu	Pro	Cys	Asp	Gly	485	490	495	
Ala	Val	Thr	Pro	Arg	Asp	Arg	Arg	Lys	His	Arg	Pro	Arg	Val	Met	Thr	500	505	510	
Leu	Pro	Pro	Cys	Pro	Pro	Asp	Met	Asp	Leu	Met	Ile	Glu	Ala	Lys	Asp	515	520	525	
Lys	Glu	Gln	Ala	Val	Phe	Glu	Leu	Met	Arg	Thr	Phe	Lys	Leu	Pro	Gly	530	535	540	
Phe	Glu	Lys	Ile	Asn	Asp	Met	Val	Pro	Tyr	Asp	Arg	Asp	Asp	Glu	Asn	545	550	555	560
Arg	Pro	Ala	Pro	Pro	Val	Lys	Ala	Pro	Lys	Lys	Lys	Lys	Gly	Gly	Lys	565	570	575	
Arg	Lys	Arg	Thr	Thr	Asp	Glu	Glu	Ala	Ala	Glu	Pro	Glu	Glu	Val	Asp	580	585	590	
Thr	Ala	Ala	Asp	Asp	Val	Lys	Asp	Ala	Pro	Glu	Gly	Pro	Lys	Glu	Val	595	600	605	
Pro	Glu	Glu	Glu	Arg	Ala	Met	Gly	Gly	Pro	Tyr	Asn	Arg	Val	Tyr	Trp	610	615	620	
Pro	Leu	Gly	Cys	Glu	Glu	Trp	Leu	Lys	Pro	Lys	Lys	Arg	Glu	Val	Lys	625	630	635	640
Lys	Gly	Lys	Val	Pro	Glu	Glu	Val	Glu	Asp	Glu	Gly	Glu	Phe	Asp	Gly	645	650	655	

<210> 37  
 <211> 317  
 <212> PRT  
 <213> Bacillus subtilis

<400> 37  
 Met Ile Phe Arg Phe Gly Phe Val Ser Asn Ala Met Ser Leu Trp Asp  
           1                  5                  10                  15  
 Ala Ser Pro Ala Lys Thr Leu Thr Phe Ala Arg Tyr Ser Lys Leu Ser  
                   20                  25                  30  
 Lys Thr Glu Arg Lys Glu Ala Leu Leu Thr Val Thr Lys Ala Asn Leu  
                   35                  40                  45  
 Arg Asn Thr Met Arg Thr Leu His Tyr Ile Ile Gly His Gly Ile Pro  
           50                  55                  60  
 Leu Tyr Arg Phe Ser Ser Ser Ile Val Pro Leu Ala Thr His Pro Asp  
           65                  70                  75                  80  
 Val Met Trp Asp Phe Val Thr Pro Phe Gln Lys Glu Phe Arg Glu Ile  
                   85                  90                  95  
 Gly Glu Leu Val Lys Thr His Gln Leu Arg Thr Ser Phe His Pro Asn  
                   100                  105                  110  
 Gln Phe Thr Leu Phe Thr Ser Pro Lys Glu Ser Val Thr Lys Asn Ala  
           115                  120                  125  
 Val Thr Asp Met Ala Tyr His Tyr Arg Met Leu Glu Ala Met Gly Ile  
           130                  135                  140  
 Ala Asp Arg Ser Val Ile Asn Ile His Ile Gly Gly Ala Tyr Gly Asn  
           145                  150                  155                  160  
 Lys Asp Thr Ala Thr Ala Gln Phe His Gln Asn Ile Lys Gln Leu Pro  
                   165                  170                  175  
 Gln Glu Ile Lys Glu Arg Met Thr Leu Glu Asn Asp Asp Lys Thr Tyr  
                   180                  185                  190  
 Thr Thr Glu Glu Thr Leu Gln Val Cys Glu Gln Glu Asp Val Pro Phe  
           195                  200                  205  
 Val Phe Asp Phe His His Phe Tyr Ala Asn Pro Asp Asp His Ala Asp  
           210                  215                  220

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Leu Asn Val Ala Leu Pro Arg Met Ile Lys Thr Trp Glu Arg Ile Gly  
225 230 235 240

Leu Gln Pro Lys Val His Leu Ser Ser Pro Lys Ser Glu Gln Ala Ile  
245 250 255

Arg Ser His Ala Asp Tyr Val Asp Ala Asn Phe Leu Leu Glu Arg Phe  
260 265 270

Arg Gln Trp Gly Thr Asn Ile Asp Phe Met Ile Glu Ala Lys Gln Lys  
275 280 285

Asp Lys Ala Leu Leu Arg Leu Met Asp Glu Leu Ser Ser Ile Arg Gly  
290 295 300

Val Lys Arg Ile Gly Gly Gly Ala Leu Gln Trp Lys Ser  
305 310 315

<210> 38

<211> 580

<212> PRT

<213> Homo sapiens

<400> 38

Met Gly Thr Thr Gly Leu Glu Ser Leu Ser Leu Gly Asp Arg Gly Ala  
1 5 10 15

Ala Pro Thr Val Thr Ser Ser Glu Arg Leu Val Pro Asp Pro Pro Asn  
20 25 30

Asp Leu Arg Lys Glu Asp Val Ala Met Glu Leu Glu Arg Val Gly Glu  
35 40 45

Asp Glu Glu Gln Met Met Ile Lys Arg Ser Ser Glu Cys Asn Pro Leu  
50 55 60

Leu Gln Glu Pro Ile Ala Ser Ala Gln Phe Gly Ala Thr Ala Gly Thr  
65 70 75 80

Glu Cys Arg Lys Ser Val Pro Cys Gly Trp Glu Arg Val Val Lys Gln  
85 90 95

Arg Leu Phe Gly Lys Thr Ala Gly Arg Phe Asp Val Tyr Phe Ile Ser  
100 105 110

Pro Gln Gly Leu Lys Phe Arg Ser Lys Ser Ser Leu Ala Asn Tyr Leu  
115 120 125

His Lys Asn Gly Glu Thr Ser Leu Lys Pro Glu Asp Phe Asp Phe Thr  
130 135 140

09724256 "052701

Val	Leu	Ser	Lys	Arg	Gly	Ile	Lys	Ser	Arg	Tyr	Lys	Asp	Cys	Ser	Met	145	150	155	160
Ala	Ala	Leu	Thr	Ser	His	Leu	Gln	Asn	Gln	Ser	Asn	Asn	Ser	Asn	Trp	165	170	175	
Asn	Leu	Arg	Thr	Arg	Ser	Lys	Cys	Lys	Lys	Asp	Val	Phe	Met	Pro	Pro	180	185	190	
Ser	Ser	Ser	Ser	Glu	Leu	Gln	Glu	Ser	Arg	Gly	Leu	Ser	Asn	Phe	Thr	195	200	205	
Ser	Thr	His	Leu	Leu	Leu	Lys	Glu	Asp	Glu	Gly	Val	Asp	Asp	Val	Asn	210	215	220	
Phe	Arg	Lys	Val	Arg	Lys	Pro	Lys	Gly	Lys	Val	Thr	Ile	Leu	Lys	Gly	225	230	235	240
Ile	Pro	Ile	Lys	Lys	Thr	Lys	Lys	Gly	Cys	Arg	Lys	Ser	Cys	Ser	Gly	245	250	255	
Phe	Val	Gln	Ser	Asp	Ser	Lys	Arg	Glu	Ser	Val	Cys	Asn	Lys	Ala	Asp	260	265	270	
Ala	Glu	Ser	Glu	Pro	Val	Ala	Gln	Lys	Ser	Gln	Leu	Asp	Arg	Thr	Val	275	280	285	
Cys	Ile	Ser	Asp	Ala	Gly	Ala	Cys	Gly	Glu	Thr	Leu	Ser	Val	Thr	Ser	290	295	300	
Glu	Glu	Asn	Ser	Leu	Val	Lys	Lys	Lys	Glu	Arg	Ser	Leu	Ser	Ser	Gly	305	310	315	320
Ser	Asn	Phe	Cys	Ser	Glu	Gln	Lys	Thr	Ser	Gly	Ile	Ile	Asn	Lys	Phe	325	330	335	
Cys	Ser	Ala	Lys	Asp	Ser	Glu	His	Asn	Glu	Lys	Tyr	Glu	Asp	Thr	Phe	340	345	350	
Leu	Glu	Ser	Glu	Glu	Ile	Gly	Thr	Lys	Val	Glu	Val	Val	Glu	Arg	Lys	355	360	365	
Glu	His	Leu	His	Thr	Asp	Ile	Leu	Lys	Arg	Gly	Ser	Glu	Met	Asp	Asn	370	375	380	
Asn	Cys	Ser	Pro	Thr	Arg	Lys	Asp	Phe	Thr	Gly	Glu	Lys	Ile	Phe	Gln	385	390	395	400
Glu	Asp	Thr	Ile	Pro	Arg	Thr	Gln	Ile	Glu	Arg	Arg	Lys	Thr	Ser	Leu	405	410	415	

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Tyr Phe Ser Ser Lys Tyr Asn Lys Glu Ala Leu Ser Pro Pro Arg Arg  
420 425 430

Lys Ala Phe Lys Lys Trp Thr Pro Pro Arg Ser Pro Phe Asn Leu Val  
435 440 445

Gln Glu Thr Leu Phe His Asp Pro Trp Lys Leu Leu Ile Ala Thr Ile  
450 455 460

Phe Leu Asn Arg Thr Ser Gly Lys Met Ala Ile Pro Val Leu Trp Lys  
465 470 475 480

Phe Leu Glu Lys Tyr Pro Ser Ala Glu Val Ala Arg Thr Ala Asp Trp  
485 490 495

Arg Asp Val Ser Glu Leu Leu Lys Pro Leu Gly Leu Tyr Asp Leu Arg  
500 505 510

Ala Lys Thr Ile Val Lys Phe Ser Asp Glu Tyr Leu Thr Lys Gln Trp  
515 520 525

Lys Tyr Pro Ile Glu Leu His Gly Ile Gly Lys Tyr Gly Asn Asp Ser  
530 535 540

Tyr Arg Ile Phe Cys Val Asn Glu Trp Lys Gln Val His Pro Glu Asp  
545 550 555 560

His Lys Leu Asn Lys Tyr His Asp Trp Leu Trp Glu Asn His Glu Lys  
565 570 575

Leu Ser Leu Ser  
580

<210> 39

<211> 294

<212> PRT

<213> Deinococcus radiodurans

<400> 39

Gln Leu Gly Leu Val Cys Leu Thr Val Gly Pro Glu Val Arg Phe Arg  
1 5 10 15

Thr Val Thr Leu Ser Arg Tyr Arg Ala Leu Ser Pro Ala Glu Arg Glu  
20 25 30

Ala Lys Leu Leu Asp Leu Tyr Ser Ser Asn Ile Lys Thr Leu Arg Gly  
35 40 45

Ala Ala Asp Tyr Cys Ala Ala His Asp Ile Arg Leu Tyr Arg Leu Ser  
50 55 60

Ser Ser Leu Phe Pro Met Leu Asp Leu Ala Gly Asp Asp Thr Gly Ala  
 65 70 75 80  
 Ala Val Leu Thr His Leu Ala Pro Gln Leu Leu Glu Ala Gly His Ala  
 85 90 95  
 Phe Thr Asp Ala Gly Val Arg Leu Leu Met His Pro Glu Gln Phe Ile  
 100 105 110  
 Val Leu Asn Ser Asp Arg Pro Glu Val Arg Glu Ser Ser Val Arg Ala  
 115 120 125  
 Met Ser Ala His Ala Arg Val Met Asp Gly Leu Gly Leu Ala Arg Thr  
 130 135 140  
 Pro Trp Asn Leu Leu Leu Leu His Gly Gly Lys Gly Gly Arg Gly Ala  
 145 150 155 160  
 Glu Leu Ala Ala Leu Ile Pro Asp Leu Pro Asp Pro Val Arg Leu Arg  
 165 170 175  
 Leu Gly Leu Glu Asn Asp Glu Arg Ala Tyr Ser Pro Ala Glu Leu Leu  
 180 185 190  
 Pro Ile Cys Glu Ala Thr Gly Thr Pro Leu Val Phe Asp Ala His His  
 195 200 205  
 His Val Val His Asp Lys Leu Pro Asp Gln Glu Asp Pro Ser Val Arg  
 210 215 220  
 Glu Trp Val Leu Arg Ala Arg Ala Thr Trp Gln Pro Pro Glu Trp Gln  
 225 230 235 240  
 Val Val His Leu Ser Asn Gly Ile Glu Gly Pro Gln Asp Arg Arg His  
 245 250 255  
 Ser His Leu Ile Ala Asp Phe Pro Ser Ala Tyr Ala Asp Val Pro Gln  
 260 265 270  
 Ile Glu Val Glu Ala Lys Gly Lys Glu Glu Ala Ile Ala Ala Leu Arg  
 275 280 285  
 Leu Met Ala Pro Phe Lys  
 290

<210> 40  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

09724296-0524260

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 40

cacagactcc ctctgtcata ggtttgagtt tatatggaa

39

<210> 41

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 41

ttccatataa actcaaacct atgacagagg gagtctgtg

39

<210> 42

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 42

cacagactcc ctctgtcata ggttcatgag tttatatgga a

41

<210> 43

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 43

cacagactcc ctctgtcata ggttcacatg agtttatatg gaa

43

<210> 44

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

09724296-052704

<400> 44  
cacagactcc ctctgtcata gggtcacaca tgagtttata tggaa 45

<210> 45  
<211> 47  
<212> DNA  
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Oligonucleotide

<400> 45  
cacagactcc ctctgtcata gggtcacaca catgagttta tatggaa 47

<210> 46  
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Oligonucleotide

<400> 46  
cacagactcc ctctgtcata gggtgagtac tagtactctg agtttatatg gaa 53

<210> 47  
<211> 41  
<212> DNA  
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<220>  
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Oligonucleotide

<400> 47  
cgttagaact ccgtcacgaa ttaagcaatt agtaatgcat t 41

<210> 48  
<211> 41  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 48  
aatgcattac taattgctta attcgtgacg gagttctaac g 41

<210> 49  
<211> 43  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 49 43  
cgttagaact ccgtcacgaa ttaagcaatt caagtaatgc att

<210> 50  
<211> 45  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 50 45  
cgttagaact ccgtcacgaa ttaagcaatt cacaaagtaat gcatt

<210> 51  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 51 47  
cgttagaact ccgtcacgaa ttaagcaatt cacacaagta atgcatt

<210> 52  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 52 49  
cgttagaact ccgtcacgaa ttaagcaatt cacacacaag taatgcatt

<210> 53  
<211> 41  
<212> DNA

09724296 052701  
"02250" 9624260

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 53

cgttacaagt ccgtcacgaa ttaagcaatt cgtaacgcat t

41

<210> 54

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 54

aatgcattac gaattgctta attcgtgacg gacttgtaac g

41

<210> 55

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 55

cgttacaagt ccgtcacgaa ttaagcaatt cgtaacgcat t

41

<210> 56

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 56

aatgcgttac aaattgctta attcgtgacg gacttgtaac g

41

<210> 57

<211> 41

<212> DNA

<213> Artificial Sequence

<220>



<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 57  
cgttacaagt ccgtcacgaa ttaagcaatt cgtaacgcat t 41

<210> 58  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 58  
aatgcggttac gaattactta attcgtgacg gacttgtaac g 41

<210> 59  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 59  
cgttacaagt ccgtcacgac ttaagcaatt cgtaacgcat t 41

<210> 60  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 60  
aatgcggttac gaattgctta aatcgtgacg gacttgtaac g 41

<210> 61  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

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T02250"9624260

<400> 61  
cgttacaagt ccgtcacgaa ttaagcaatt cgtaacgcat t 41

<210> 62  
<211> 41  
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<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 62  
aatgcgttac gaattgctta attcgtaacg gacttgtaac g 41

<210> 63  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 63  
cgttacaagc ccgtcacgaa ttaagcaatt cgtaacgcat t 41

<210> 64  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 64  
aatgcgttac gaattgctta attcgtgacg gacttgtaac g 41

<210> 65  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 65  
cgttccaagt ccgtcacgaa ttaagcaatt cgtaacgcat t 41

<210> 66  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 66  
aatgcgttac gaattgctta attcgtgacg gacttgaaac g 41

<210> 67  
<211> 78  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 67  
tgcacggacc tcgagagaac cgaacgatcc ggatgtgatc atgggacaga attcgcacac 60  
tgcactcgac gatagtct 78

<210> 68  
<211> 49  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 68  
tgcagtgtgc gaattctgtc ccatcatcac atccggatcg ttcggttct 49

<210> 69  
<211> 62  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 69  
gactatcgtg cagtgcagtg tgcgaattct gtcccatcat cacatccgga tcgttcggtt 60  
ct 62

<210> 70

<211> 64  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 70  
tgcagtgtgc gaattctgtc ccatcatcac atccggatcg ttcggttctc tcgaggtccg 60  
tgca 64

<210> 71  
<211> 79  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 71  
gagactatcg tgcagtgcag tgtgcgaatt ctgtcccatc atcacatccg gatcgttcgg 60  
ttctctcgag gtccgtgca 79

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T02250" 9624260